Data 583 Life Expectancy (WHO)

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Data 583 Life Expectancy - Final Report (Life Expectancy Data)

Part 1. Introduction and Hypotheses

Life Expectancy has always been an area of interest for humanity. The dataset contains the Life Expectancy records of 193 countries between 2000-2015, together with different predictive factors. Broadly speaking, predicting variables are categorized into 4 major areas : Immmunization, Mortality, Economical, and Social, containing a total of 21 individual variables.

The primary purpose of this report is to compare and evaluate different predictive models in order to identify the most appropriate model for the dataset. In particular, we will evaluate the applicability of the core assumptions of the selected models by methods such as Normality Test, Multicollinearity Assessment, etc. This could validate or decline the adoption of certain models because the model assumptions are simply not satisfied. We are also going to verify whether the 4 predicting areas have equal significance on Life Expectancy, and whether there are adequate support evidence suggesting a strong correlation with the response variables. Finally, we will also perform and compare fitting result of selected models, in particular whether parametric models would be more suitable than non-parametric models for this dataset.

Part 2. Dataset overview

Varaibles Types

Variable	Unit of Measurement/Data Category	Continuous vs Discrete
Life Expectancy	Years Old (Age)	Continuous
Country	Nominal Data	Discrete
Year	Ordinal Data	Discrete
Status	Nominal Data	Discrete
Adult Mortality	Count Data	Discrete
Infant deaths	Count Data	Discrete
Under-five deaths	Count Data	Discrete
Hepatitis B	Percentage	Continuous
Measles	Count Data	Discrete
Polio	Percentage	Continuous
Diphtheria	Percentage	Continuous
Total expenditure	Percentage	Continuous
Percentage expenditure	Percentage	Continuous
GDP	Currency (USD)	Continuous
Population	Count	Discrete
Income composition of resources	Percentage	Continuous
Schooling	Mean (Years)	Continuous

Variable	Unit of Measurement/Data Category	Continuous vs Discrete
Alcohol	Litres	Continuous
HIV/AIDS	Percentage	Continuous
BMI	Average BMI	Continuous
Thinness 1-19 years	Percentage	Continuous
Thinness 5-9 years	Percentage	Continuous

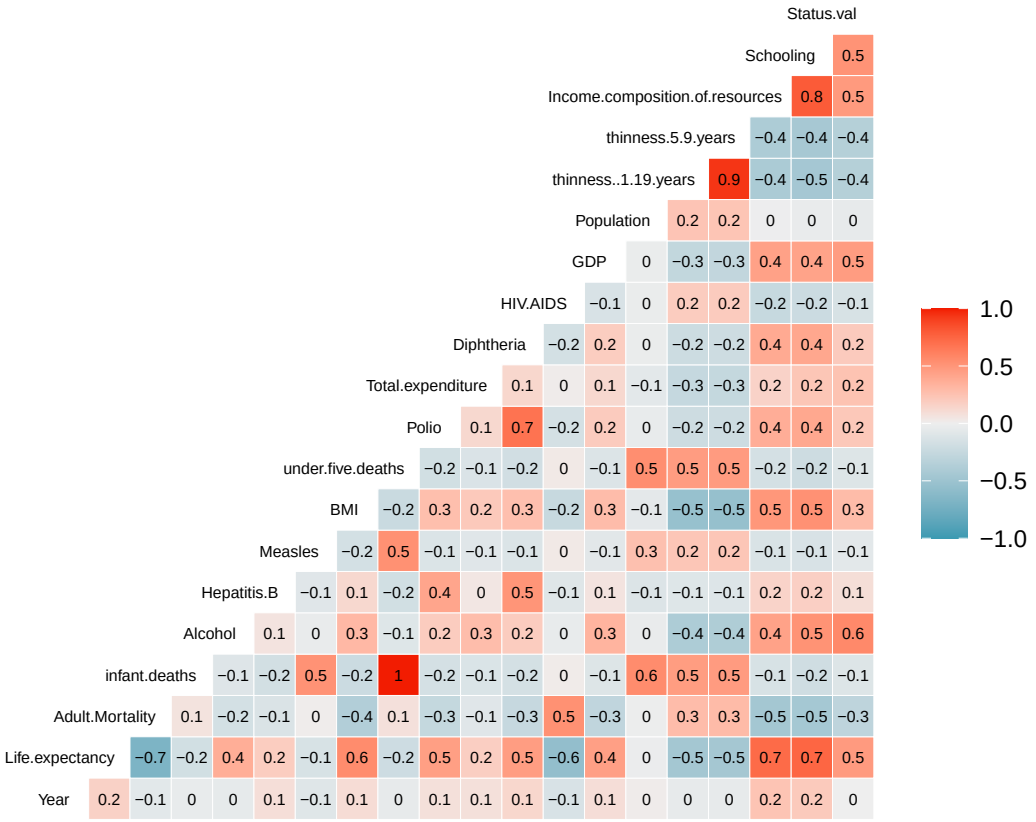
Variables Summary and Categories

Life Expectancy is the response variable in this dataset. This represents the mean of the life expectancy (in age) in a specific country in a given year. For the data types of the predicting variables, most are percentage and count data across four major areas. The first area is Immunization Data such as Hepatitis B and Polio (immunization coverage). The second area is Mortality Data such as Adult Mortality/infant deaths (No. of deaths of Adult/infant per 1000 persons). The third area is Economical Data such as GDP/Income composition/Percentage expenditure. The fourth area is Social Data such as Schooling and Population.

To clean up and wrangle data for the subsequent analysis, NA data has been assessed. A total of 2563 NA values are found in the dataset, spreading across a few columns. These NA values are generally imputed by the respective column mean.

Checking for Multicollinearity

As Multicollinearity can potentially affect the accuracy of regression model and we have 22 variables, a correlation study is undertaken to understand and assess the situation. A correlation plot has identified a number of correlation problems. It is found that infant deaths and under.five.deaths are nearly 100% correlated. The relation between the deaths rates of the two close age groups is easily interpretable. In addition, there are three heavily correlated pairs which is defined by the abs(correlation coefficient)>0.7 between the variables. They include (a) (immunization rate of) 'Polio'-vs-'Diphtheria', (b) 'income composition of resources'-vs-'Schooling', and (c) between the two thinness measures for the age groups 5-9 vs 10-19. Pairs (a) and (c) are justifiable while the relation for (b) demonstrate a relatively subtle relation. Other than that, the degree of multicollinearity is acceptable and not too worrying.



Variables Selection

Due to the above correlations between certain variables, in addition to a large number of variables in our model, a variable selection is conducted to remove some correlated variables and attain a simpler model via variable selection. A BIC backward step model selection method has been applied to the dataset, with the following summary :

Models	No. of Variables	AIC Score	Adj R-squared Score
Original Model	20	7642.14	0.8299
Reduced Model	12	7604.24	0.8296

The reduced model now contains the following variables : Adult.Mortality + infant.deaths + Hepatitis.B + BMI + under.five.deaths + Polio + Diphtheria + HIV.AIDS + GDP + thinness..1.19.years + Income.composition.of.resources + Schooling

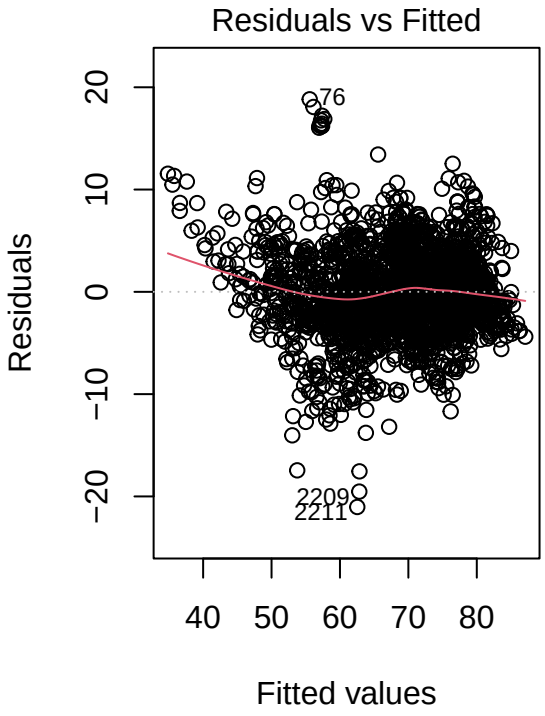
The number of independent variables are now effectively reduced to 12, together with a lower AIC score of 7604.34. Meanwhile, the adjusted R-squared score is well kept at nearly the same level as in the original model. We are satisfied with the performance of this reduced model. This reduced model will therefore be adopted as the basis for further analysis in this report.

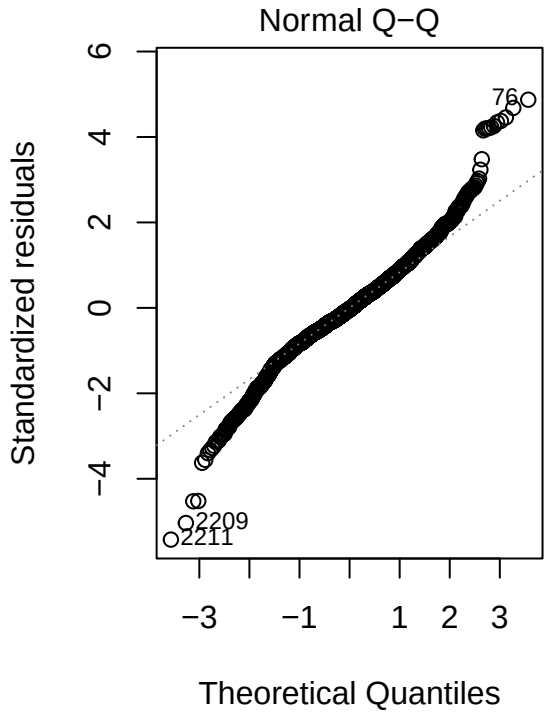
We eliminate the Status variable from the selected list of variables in the reduced model as this is a factor variable with two statuses and not continuous. We first study the effect of the model without this variable.

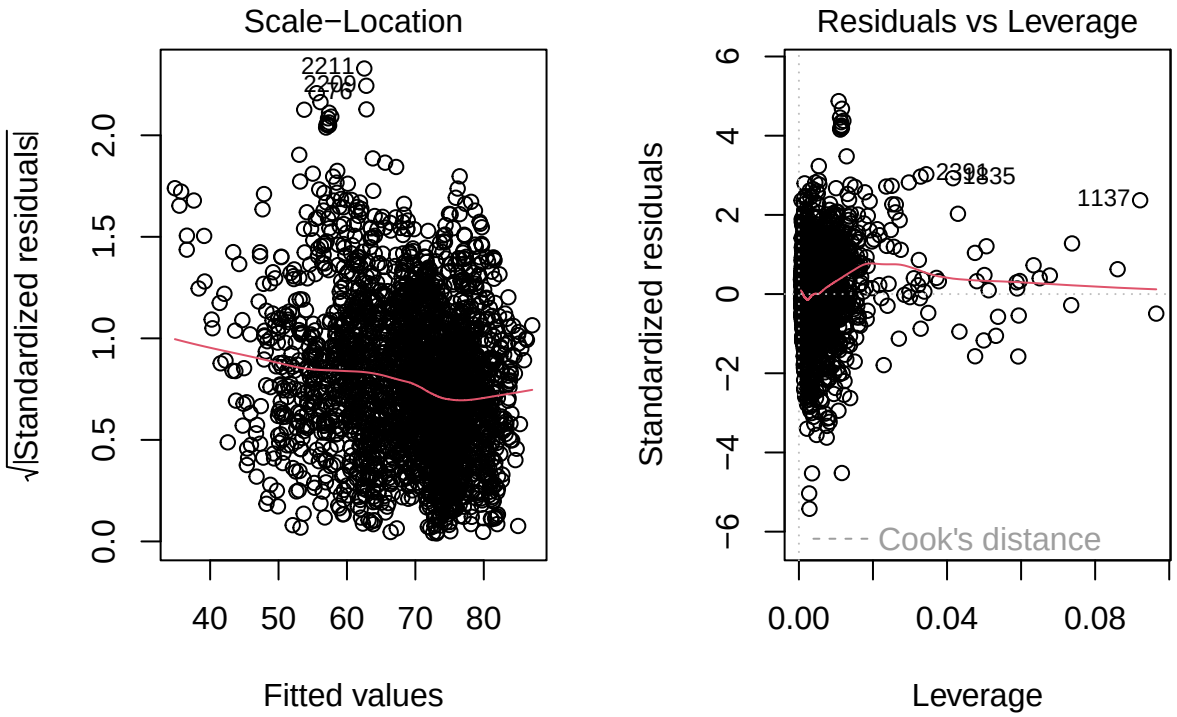
Part 3. Regression Analysis

Linear model and diagnostics

The initial model shows that we are able to explain approximately 82% of variability of our response variable using the selected predictor variables. The next step is to look at the error diagnostics from the model.



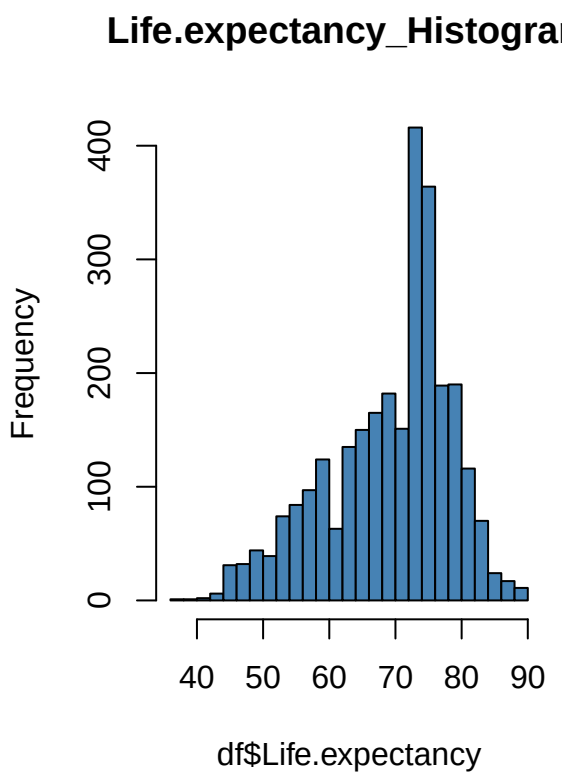




The QQ plot suggests that the model is heavy tailed and the data on both ends of the quantiles do not fit on a straight line. This is an indication that the current linear regression based model is not fitting the data well. Based on this, we undertake some additional testing to validate if the model is adequate and valid

```
#Histogram & QQPlot
par(mfrow=c(1,2))
hist(df$Life.expectancy, col='steelblue', main='Life.expectancy_Histogram',breaks = 35)
#not really a good "bell-shape"
#qqnorm(df$Life.expectancy, main='Life.expectancy_QQplot')
#S #most of the data is not fall along a straight diagonal line
#qqline(df$Life.expectancy)

#Both are indicating that our predict variable Y "df$Life.expectancy" is not normally distributed
```



a. Life expectancy variable distribution

From the histogram, it can be noticed that the response variable life expectancy is not normally distributed. From the plot, it also seems like a bimodal distribution of life expectancy data in the dataset.

b. Normal distribution test for our y variable Next, we evaluate to confirm if the response variable is normally distributed using Shapiro-Wilk test. The test has a p-value that is very small and is less than 0.05, this indicates that our response variable if not normally distributed.

```
#Shapiro-Wilk Test

shapiro.test(df$Life.expectancy)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df$Life.expectancy
## W = 0.95676, p-value < 2.2e-16
```

```
#Finding: Since df$Life.expectancy p-value is less than .05, indicate that our y variable is not normally
```

c. Parametric model specification tests Another test to see if the above parametric model specification is correct.

```
library(lmtest)
```

```
## Warning: package 'lmtest' was built under R version 4.2.2
```

```
## Loading required package: zoo

## Warning: package 'zoo' was built under R version 4.2.2

##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
resettest(lmmod2)
```

```
##
##  RESET test
##
## data:  lmmod2
## RESET = 121.2, df1 = 2, df2 = 2763, p-value < 2.2e-16
```

d. np specification test

```
##
## Consistent Model Specification Test
## Parametric null model: lm(formula = Life.expectancy ~ Adult.Mortality +
##                           infant.deaths + Hepatitis.B + BMI + under.five.deaths
##                           + Polio + Diphtheria + HIV.AIDS + GDP +
##                           thinness..1.19.years +
##                           Income.composition.of.resources + Schooling, data =
##                           df, x = TRUE, y = TRUE)
## Number of regressors: 12
## IID Bootstrap (399 replications)
##
## Test Statistic 'Jn': 21.17521    P Value: < 2.22e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Null of correct specification is rejected at the 0.1% level
```

All the diagnostic tests indicate that linear regression is not an appropriate model for the given data as assumptions for the model are violated.

Parametric model and assessments

As the linear model is not adequate, we move on to model this with other models that do not assume normal distribution. The models selected for the given dataset are LASSO and Neural Net with linear activation function. The following variables are selected for rest of the modeling based on correlation of the variables with the response variable and our knowledge on the domain. Here is a summary of the variable selection and our comments.

Need to add a table

Two different supervised algorithms tried on the dataset. They do not have the constraint of a normal distribution for response variable.

First did a train and test split so we can measure the MSE and compare how each of the models are performing in terms of minimizing MSE.

Test MSE comparison for the three models

Need to add a table

```
print(mselm_te1)
```

```
## [1] 15.84525
```

```
print(mselas_te1)
```

```
## [1] 15.87835
```

```
print(min(mse_nnet_lin))
```

```
## [1] 24.95673
```

```
#MSE comparison
```

As we compare linear model, lasso and neural net, we see that the test MSE is minimum for LASSO model. So this is a model that can be considered for the dataset.

Nonparametric regression

The response variable shows a bimodal distribution and nonparametric regression performs better on such datasets per literature. We next try non parametric regression on the dataset.

```
library(np)
# n <- names(df)
# f <- as.formula(paste("df$Life.expectancy ~", paste(n[!n %in% "Life.expectancy"], collapse = " + ")))
#
# model_np <- npregbw(Life.expectancy ~ Adult.Mortality + infant.deaths + Hepatitis.B + BMI + under.five.d

# model_np <- npreg(bws = model_np)
# summary(model_np)
model_np <- readRDS("model_np.rds") #PreTrained Model
summary(model_np)
```

```
##
## Regression Data: 2778 training points, in 12 variable(s)
##                Adult.Mortality infant.deaths Hepatitis.B      BMI
## Bandwidth(s):       389457535       6733757   225092161 79216285
##                under.five.deaths   Polio Diphtheria HIV.AIDS          GDP
## Bandwidth(s):          95308072 5825954   19248839 1.393258 167351562078
##                thinness..1.19.years Income.composition.of.resources Schooling
## Bandwidth(s):             37667667                         1071202  15165344
##
## Kernel Regression Estimator: Local-Linear
## Bandwidth Type: Fixed
## Residual standard error: 3.345092
## R-squared: 0.8722143
##
## Continuous Kernel Type: Second-Order Gaussian
## No. Continuous Explanatory Vars.: 12
```

We see that the R^2 is increased to 87% approximately. Done with local linear estimator and cv.aic. This is a cross validated model and help estimate the long run performance. Can we see BIC?

```
#npsigtest_npreg <- npsigtest(model_np)    #10 HRs to run...
```

```
> npsigtest(model_np)

Kernel Regression Significance Test
Type I Test with IID Bootstrap (399 replications, Pivot = TRUE, joint = FALSE)
Explanatory variables tested for significance:
Adult.Mortality (1), infant.deaths (2), Hepatitis.B (3), BMI (4), under.five.deaths (5), Polio (6), Diphtheria (7), HIV.AIDS (8),
 GDP (9), thinness..1.19.years (10), Income.composition.of.resources (11), Schooling (12)

             Adult.Mortality infant.deaths
Bandwidth(s):       389457535       6733757
             Hepatitis.B      BMI under.five.deaths
Bandwidth(s):   225092161 79216285          95308072
               Polio Diphtheria HIV.AIDS
Bandwidth(s): 5825954   19248839 1.393258
                       GDP thinness..1.19.years
Bandwidth(s): 167351562078              37667667
             Income.composition.of.resources
Bandwidth(s):                         1071202
             Schooling
Bandwidth(s):  15165344

Individual Significance Tests
P Value:
Adult.Mortality                 < 2e-16 ***
infant.deaths                   < 2e-16 ***
Hepatitis.B                     0.047619 *
BMI                             < 2e-16 ***
under.five.deaths               < 2e-16 ***
Polio                           < 2e-16 ***
Diphtheria                      < 2e-16 ***
HIV.AIDS                        < 2e-16 ***
GDP                             < 2e-16 ***
thinness..1.19.years            < 2e-16 ***
Income.composition.of.resources < 2e-16 ***
Schooling                       < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 1: npsigtest_npreg result

We measure the significance of the variables for a parsimonious model. All the parameters used are significant.

Summarizing the different models and the performance assessed during the course of this project #### Add table

Model improvements

1. status variable and other ordinal, nominal variables
2. train and test split for np, but what we have now is sufficient for measuring long run performance
3. multicollinearity between the variables infant.deaths and under.five.deaths. Remove one of the variables and study if there are improvements in performance
4. measure without imputing data

Challenges

1. 30 hours for npreg
2. 30+ hours for model significance
3. null values in the dataset, columns dropped - , columns imputed with mean -

Conclusion

np and LASSO are suitable for this dataset. We find that life expectancy is. . . .